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OM protein - protein search, using sw model
                                                                           Copyright
                                                                         GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Run on: April 20, 2004, 21:52:54 ; Search time 55 Seconds (without alignments) 128.431 Million cell updates/sec

Title: Perfect score: US-10-019-482-1

Sequence: 105 д Диреалекалкуалеалекалкайд (25)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues

Searched:

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:* geneseqp1980s:*
geneseqp200s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003s:*
geneseqp2003bs:*
geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	BB	ID	Description
	101	96.2	25	4	AAB66787	Aab66787 Amphipath
2	65	61.9	104	7	ADE10685	-
× u	65	61.9	104	7	ADE10635	•
4	62.5	59.5	428	σ	ABU27824	Abu27824 Protein e
5	62	59.0	104	7	ADE10683	_
6	. 62	59.0	104	7	ADE10682	••
7	62	59.0	104	7	ADE10633	Structur
œ	62	59.0	104	7	ADE10632	••
9	61.5	58.6	104	7	ADE10684	_
10	61.5		104	7	ADE10634	Structur
11	61	58.1	59	7	ADE10698	_
12	61	58.1	59	7	ADE10648	
13	61	58.1	67	7	ADE10697	-
14	61	58.1	67	7	ADE10647	Adel0647 Structura
15	61	58.1	75	7	ADE10696	٠.
16	61	58.1	75	7	ADE10646	Adel0646 Structura
17	61	58.1	83	7	ADE10695	Ade10695 Structura
18	61	58.1	83	7	ADE10645	٠.
19	61	58.1	88	7	ADE10642	Ade10642 Structura
20	61	58.1	88	7	ADE10692	Adel0692 Structura
21	61	58.1	91	7	ADE10694	Adel0694 Structura
22	61	58.1	91	7	ADE10644	Adel0644 Structura
23	61	58.1	104	7	ADE10690	_
24	61	58.1	104	7	ADE10640	_
25	61	58. -1	1	ı		

45	44	43	42	41	_		38	37	36	35	34	33	32	31	30	29	28	27	26
58	58	58	58	58	59	59.5	60	60	61	61	61	61	61	19	61	61	61	61	61
55.2	55.2	55.2	55.2	55.2	56.2	56.7	57.1	57.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	æ	58.1	58.1	œ
104	104	104	78	78	421	56	33	ω u	700	623	111	110	106	106	106	106	106	106	105
7	7	7	7	7	თ	w	N	N	σ	D	7	7	7	7	7	7	7	7	7
ADE10631	ADE10680	ADE10681	ADE10616	ADE10666	ABU28559	AAY82573	AAW06688	AAR90181	ABJ26443	ABJ25843	ADE10691	ADE10641	ADE10637	ADE10638	ADE10689	ADE10687	ADE10688	ADE10639	ADE10686
Ade10631	Ade10680	Ade10681	Ade10616	Ade10666	Abu28559	Aay82573	Aaw06688	Aar90181	Abj26443	Abj25843	Ade10691	Ade10641	Ade10637	Ade10638	Ade10689	Ade10687	Ade10688	Ade10639	Ade10686
Structura	Structura	Structura	Structura	Structura	Protein e	Copolymer	Protamine	Polycatio	Aspergill	Aspergill	Structura								

ALIGNMENTS

RESULT 1 AAB66787 Synthetic. WO200102425-A2. Amphipathic; lipid bilayer; detergent. Amphipathic peptide conjugate AAB66787; AAB66787 standard; peptide; 11-APR-2001 (first entry) 25 AA.

11-JAN-2001.

29-JUN-2000; 2000WO-CA000773

29-JUN-1999; 99US-0140988P

(UYHE-) UNIV HEALTH NETWORK.

Prive G;

WPI; 2001-138120/14.

New amphiphatic peptide conjugate having detergent properties, and hydrophobic and hydrophilic phase, useful e.g. for stabilizing and crystallizing proteins and membrane proteins, as cytolytic agents, surfactants or emulsifiers.

Claim 1; Page 22; 29pp; English.

The present invention relates to an amphipathic peptide conjugate having detergent properties and a hydrophobic and hydrophilic face. The amphipathic peptide conjugate may be used for the stabilization and crystallization of proteins and membrane proteins, for modifying the properties of lipid bilayer membranes, as cytolytic agents, as molecules that can facilitate the transport of polar molecules across biological membranes, and as emulsifiers and surfactants

Sequence 25 AA;

Query Match
Best Local Similarity
Matches 25; Conserv 96.2%; Somilarity 100.0%; For Conservative 0; Score 101; DB 4; ; Pred. No. 2.7e-07; 0; Mismatches 0; Length 25; Indels 0; Gaps

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RESULT 2
ADE10685
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         CC peptides conferring a change in specific phenotype such as cell cells, and cellular density; changes in the expression of one or more CR cells, and cellular density; changes in the expression of one or more CR NAMs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAS, protein, CI lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAS, protein, CI lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more CC candidate peptides and to identify target molecules, i.e., the molecules combined with other pharmacologic activators to study the epistatic CC combined with other pharmacologic activators to study the epistatic CC relationships of signal transduction pathways in question. The disclosed CC introduced into any tumour cell (primary or cultured), and peptides CC identified which by themselves induce apoptosis, cell death, loss of cell CC division or decreased cell growth. The method is also useful for CC screening of bioactive peptides which restore the constitutive function CC of the brca-1 or brca-2 genes, and other tumour suppressor genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discas-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a library (I) of fusion nucleic acids, where extusion nucleic acid comprises a first nucleic acid (NI), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical blasing sequence; where NI is fused to N2. Disclosed is a method for screening bioactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 92; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-829786/77.
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99US-00415765.
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RESULT 3
ADE10635
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APC) and the Drosophila discs-large gene (DIg), which are cell-cell junctions. The methods are useful in cardiovascul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structurally biased random peptide library related protein seqid 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE10635 standard; protein;
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                                                                                                                                                                                                                                                                    08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion nucleic acid library; scaffold protein; bioactive
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17; Conserv
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99US-00415765.
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Pred. No.
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The invention describes a library (I) of fusion nucleic acids, whe fusion nucleic acid comprises a first nucleic acid (N1), encoding scaffold protein sequence; and a second nucleic acid (N2), encoding library peptide sequence comprising an alpha helical biasing sequence.

Example

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NO 42;

110pp;

English

Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lapha helical biasing sequence, respectively, useful in screening

where N1 is fused to N2. DISCLUSE 15 a MULTIPLE SUCH AS CELL peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, or other molecules; etc. The bioactive

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ID ABUZ
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Matches
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                                                                                                                                21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacter cloacae
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                                                                        (ELIT-)
                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #13351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU27824 standard;
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                                                                 ELITRA PHARM
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                                                                     INC.
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Pred. No. 0.12;
0; Mismatches
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Sequence 428

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Wang L,

Zamudio C,

Malone C,

Haselbeck

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Ohlsen KL,

Zyskind JW,

scaffold protein.

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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense concluded acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fredgment whose expression is inhibited by the antisense concluded acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibited by the containing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway of the gene product or that has an activity against a biological pathway of containing a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the contains or screening for homologous nucleic acids required that of a contain a contain a contain a contain and activity acids.
                                                                                                                                                                                                                                                                                               for cellular proliferation to tortion than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells of the cel
                                                                              K. pneumoniae or P. aeruginosa. The present sequence is encoded by one the target prokaryotic essential genes. Note: The sequence data for thi patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                              CC fusion nucleic acid comprises a first nucleic acid (NI); encoding a cc saffold protein sequence; and a second nucleic acid (NI); encoding a cc library peptide sequence comprising an alpha helical biasing sequence; cc where NI is fused to NZ. Disclosed is a method for screening bicactive comprises conferring a change in specific phenotype such as cell comprised conferring a change in specific phenotype such as cell comprised conferring a change in specific phenotype such as cell in the expression of one or more comprised in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; changes in the expression of one or more comprised identified by above mentioned method is used to generate more comprised identified by above mentioned method is used to generate more comprised with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides can be cintroduced into any tumour cell (primary or cultured). The epistatic components of coff the broad or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function coff the broad or broad genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coll gene (APC) and the brosophila dises-large gene (DI), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin collaborations, inmunobiology, inflammation, and allergic resistance applications, inmunobiology, inflammation, and allergic classes applications, made because a protein used in generate elevated celluar concentration of structurally biased libraries generate elevated collaborative generat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having
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08-OCT-1999;
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                                                                                                                                                            Sequence 104 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha helical biasing sequence, respectively, useful in screening
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llarity 72.0%;
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99US-00415765.
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Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening

Disclosure; SEQ ID NO 89; 110pp; English

cc scaffold protein sequence; and a second nucleic acid (N2), encoding a cc library peptide sequence; and a second nucleic acid (N2), encoding a cc library peptide sequence comprising an alpha helical biasing sequence; cc where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell ccells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; ctanges in the equilibrium state (i.e., half-life) or one or more RNAs, protein, compatitie identified by above mentioned method is used to generate more combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic cidentified which by themselves induce apoptosis, cell death, loss of cell civision or decreased cell growth. The method is also useful for cidentified which by themselves induce apoptosis, cell death, loss of cell cell-cell junctions. The method is also useful for comportant in breast cancer such as the adenomatous polyposis coli gene (APC) and the Drosophila discs-large gene (DIG), which are components of cell-cell-cell junctions. The methods are useful in cardiovascular arnivations. The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology

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The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHARM INC
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99US-00415765.
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Pred. No. 0.31
0; Mismatches
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RESULT 8
ADE10632
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                                                                                                  08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                      31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structurally biased random peptide library related protein seqid 39.
               Anderson
                                                                                                                                                               20-JUN-2002; 2002US-00177725
                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                 drug toxicity;
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                                                           (RIGE-) RIGEL PHARM INC.
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               Peelle BR,
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                                                                                                                                                                                                                                                                                                                                 drug resistance; inflammation; allergic response
                                                                                                  98US-00169015.
99US-00415765.
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               Bogenberger JM;
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Pred. No. 0.31
0; Mismatches
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bioactive
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WPI; 2003-829786/77

Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening

Example 6; SEQ ID NO 39; 110pp; English

cc peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more CRNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, clipids, hormones, cytokines, or other molecules; changes competitive peptide identified by above mentioned method is used to generate more combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined combined with other pharmacologic activators to study the epistatic combined combined with other pharmacologic activators to study the epistatic combined combined because of call combined with other pharmacologic activators to study the epistatic can be constituted with other pharmacologic activators. Random libraries can be constituted with other pharmacologic activators to study the epistatic can be constituted with other pharmacologic activators. The method is also useful for constitutive function conference such as the adenomatous polyposis coli gene (APC) and the Drosophila discs-large gene (Dig), which are components of coll captions of the protein applications bone biology applications, skin collections applications bone biology applications. applications, neurobiology applications, bone biology applications, skin biology applications, cosmecceutical applications, endocrinology applications, infectious disease applications, from toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention. The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bloactive

Sequence 104 A,

18; Similarity Conservative 59.0**%**; Score 62; DB 7; Pred. No. 0.31; 0; Mismatches 0 DB 7; 5 Length 104; Indels 2; Gaps

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ADE10684 standard; protein; 104 AA

29-JAN-2004 (first entry)

Structurally biased random peptide library scaffold protein seqid

ADE10684
ADE10684
XX
AC ADE1
AC AD fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell death; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; prosophila discs-large; DIG; cardiovascular; neurobiology; bone biology bone biology

skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response; scaffold protein.

Synthetic

US2003143562-A1

20-JUN-2002; 2002US-00177725

08-OCT-1998; 08-OCT-1999; 98US-00169015 99US-00415765

(RIGE-) RIGEL PHARM INC

Ď, Peelle BR, Bogenberger JM;

WPI; 2003-829786/77.

second nucleic acids encoding scaffold protein alpha helical biasing sequence, respectively, Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening

Disclosure; SEQ ID NO 91; 110pp; English

CC candidate peptides and to identify target molecules, i.e., the molecules (candidate peptides and to identify target molecules) i.e., the molecules (cC combined with other pharmacologic activators to study the epistatic (cC crelationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be (cC introduced into any tumour cell (primary or cultured), and peptides (cd identified which by themselves induce apoptosis, cell death, loss of cell (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cd division or decreased cell growth. The method is also useful for (cell-cell) functions. The methods are useful in cardiovascular (cell-cell junctions, neurobiology applications, bone biology applications, skin biology applications, endocrinology (cell-cell functions, infectious disease applications, drug toxicities and drug (cell-cell functions), commeccutical applications, and allergic (cliptary can easily be monitored, both for its presence within cells and (cliptary can easily be monitored, both for its presence within cells and (cliptary can easily be monitored, both for its presence within cells and (cliptary can easily be monitored, both for its presence within cells and (cliptary can easily be monitored, both for its presence within cells and (cliptary can easily be monitored, both for its presence within cells and (cliptary can easily be monitored to the complete that bind such (cliptary cell decreased the hit rate for targets that bind such (clipt in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bloactive peptide identified by above mentioned method is used to generate more peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a form

Sequence 104 A,

Matches Query Match Best Local Similarity 58.6%; Score 61.5; DB Pred. No. 0.37; 0; Mismatches DB Length 104; ۲, Gaps

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RESULT 10 ADE10634 ADE10634 standard; protein; 104 (first

Structurally biased random peptide library related protein seqid 41.

fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeccutical; endocrinology; infectious disease; skin biology; cosmeccutical; endocrinology; infectious disease; drug resistance; inflammation; allergic response

31-JUL-2003

20-JUN-2002; 2002US-00177725

08-OCT-1998; 08-OCT-1999; 98US-00169015 99US-00415765

(RIGE-) RIGEL PHARM INC.

Anderson D, Peelle BR, Bogenberger JM;

Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening

Example 6; SEQ ID NO 41; 110pp; English.

CC peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, CC lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more CC candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be CC with which the bioactive peptide interacts. The peptide(s) can be CC combined with other pharmacologic activators to study the epistatic CC relationships of signal transduction pathways in question. The disclosed CC method is also useful in cancer applications. Random libraries can be CC identified which by themselves induce apoptosis, cell death, loss of cell cidentified which by themselves induce apoptosis, cell death, loss of cell components of the brca-1 or brca-2 genes, and other tumour suppressor genes CC important in breast cancer such as the adenomatous polyposis coli gene CC (APC) and the Drosophila discs-large gene (DIg), which are components of CC cell-cell junctions. The methods are useful in cardiovascular The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive

fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or othe

Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening

WPI; 2003-829786/77.

'n

Peelle BR,

Bogenberger JM

Disclosure;

SEQ

ID NO 105; 110pp; English

where each

or other

08-OCT-1998; 08-OCT-1999;

98US-00169015. 99US-00415765.

(RIGE-)

RIGEL

PHARM INC.

20-JUN-2002; 2002US-00177725

US2003143562-A1 Synthetic

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC lipids, hormones, cytokines, or other molecules; etc. The bioactive cc candidate peptide and troidentify target molecules; i.e., the molecules cC with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic cc with which the bioactive peptide interacts. The peptide(s) can be cc combined with other pharmacologic activators to study the epistatic cc method is also useful in cancer applications. Random libraries can be cc identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for cof the broa-1 or broa-2 genes, and other tumour suppressor genes cc important in breast cancer such as the adenomatous polyposis coli gene cc (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular capplications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, drug toxicities and drug cresistance applications, and biotechnology applications. The peptide cc library can easily be monitored, both for its presence within cells and cc structures. This is the amino acid sequence of a scaffold protein used in ceptide libraries ot hold the library peptide in a conformationally cc restricted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, the equilibrium state (i.e., half-life) or one or more RNAs, protein, or other molecules; etc. The bioactive
                                      08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                     tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease;
                                                                                                                                                                                                                                                                                                                           fusion nucleic acid library; scaffold protein; bloactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                Structurally biased random peptide library related protein seqid 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE10648 standard; protein; 59
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                                                                                                                                      31-JUL-2003
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                                                                                                2002US-00177725
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99US-00415765.
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0.23;
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Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                    Anderson D,
                                                                                                                                                                                                                    Peelle BR,
                                                                                                                                                                                                                    Bogenberger JM;
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Example 6; SEQ ID NO 55; 110pp; English. methods.

CC scaffold protein sequence; and a second nucleic acid (NI), encoding a cc library peptide sequence comprising an alpha helical biasing sequence; and a second nucleic acid (N2), encoding a cc library peptide sequence comprising an alpha helical biasing sequence; co cells is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell unreceived comprehology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more calls, and cellular density, changes in the expression of one or more calls, changes, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, completely, hormones, cytokines, or other molecules, i.e., that bloactive peptides and to identify target molecules, i.e., the molecules candidate peptides and to identify target molecules, i.e., the molecules with which the bloactive peptide interacts. The peptides can be combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic conference of introduced into any tumour cell (primary or cultured), and peptides cidentified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for conference of the brea-1 or brea-2 genes, and other tumour suppressor genes of cell cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, infunnobiology, inflammation, and altergic component applications, infunnobiology, inflammation, and altergic conference applications, and biotechnology applications. The peptide of its quantity. The expression of structurally biased libraries generate collaboration such associated with cells and cultivate for targets having a given structural with cells and collaboration of the invention. The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a Sequence 59 AA;

S Matches Query Match Best Local 16; Similarity Conservative 58.1%; Score 61; DB Pred. No. 0.23 0; Mismatches 0; DB 7; Length 59; Indels 0 Gaps

0

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                   AEAAEKAAKYAAEAAEKAAKAXA 25
AAAAEAAKAAAEAAAKAAAEAA 27
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                                         Χä
                                                   ADE10697
                                                       RESULT 13
                                              ADE10697 standard; protein;
                            (first
                            entry)
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fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell tumour; apoptosis; cell death;

Structurally biased random peptide library scaffold protein segid 104.

(RIGE-) RIGEL PHARM INC

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tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
scaffold protein.
                                                                                                                                                                                                                          loss of cell division;
                                                                                                                                                                                                                 decreased cell growth; brca-1; brca-2;
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US2003143562-A1.

31-JUL-2003

20-JUN-2002; 2002US-00177725

08-OCT-1998; 08-OCT-1999; 98US-00169015 99US-00415765

(RIGE-) RIGEL PHARM INC

Anderson D, Peelle BR, Bogenberger JM

WPI; 2003-829786/77

Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening having and

Disclosure; SEQ ID NO 104; 110pp; English

The invention describes a library (I) of fusion nucleic acids, where each CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a CC scaffold protein sequence; and a second nucleic acid (N2), encoding a CC library peptide sequence comprising an alpha helical biasing sequence; CC where N1 is fused to N2. Disclosed is a method for screening bloactive peptides conferring a change in specific phenotype such as cell cC morphology, cell growth, cell viability, adhesion to substrates or other CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, cc lipids, hormones, cytokines, or other molecules; etc. The bioactive cc method is dentified by above mentioned method is used to generate more cc with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic crelationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be cc introduced into any tumour cell (primary or cultured), and peptides (identified which by themselves induce apoptosis, cell death, loss of cell civision or decreased cell growth. The method is also useful for containt in breast cancer such as the adenomatous polyposis coli gene (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell cell-cell junctions. The methods are useful in cardiovascular amplications beneficiations of the methods are useful in cardiovascular amplications beneficial and interactions. applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, frug toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used in peptide libraries of hold the library peptide in a conformationally ij

Sequence 67 B

Best Local Similarity Query Match 58.1%; Score Pred. No. DB 7; 0.27; Length

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                                                                                                                                                                                                                                                                                                                                                                                              tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovasci, neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structurally biased random peptide library related
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Synthetic US2003143562-A1

31-JUL-2003

20-JUN-2002; 2002US-00177725

(RIGE-) RIGEL PHARM INC

08-OCT-1998; 08-OCT-1999;

98US-00169015. 99US-00415765.

Ō, Peelle BR; Bogenberger JM;

WPI; 2003-829786/77.

Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide halpha helical biasing sequence, respectively, useful in screening and

Example 6; SEQ ID NO 54; 110pp; English

cc peptides conferring a change in specific phenotype such as cell comorphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, clipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, clipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more combined in the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be controduced into any tumour cell (primary or cultured), and peptides introduced into any tumour cell (primary or cultured), and peptides of cereening of bioactive peptides which restore the constitutive function of the broa-1 or broa-2 genes, and other tumour suppressor genes considered constitutive function of the broa-1 or broa-2 genes, and other tumour suppressor genes The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell alhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; blg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
                                                                                                                          Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                              08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structurally biased random peptide library scaffold protein seqid 103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular
                                                                                                                                                                                               WPI; 2003-829786/77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scaffold protein.
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99US-00415765.
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                                                                                                                                                                                                                              Bogenberger JM;
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Pred. No. 0.27
0; Mismatches
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cc where N1 is fused to N2. Disclosed is a method for screening bioactive comprhology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more can be cell with the expression of one or more can be compared to the equilibrium state (i.e., half-life) or one or more expanses. Cycokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more expected to generate more can be compared to income cycokines, or other molecules, i.e., the molecules peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules can be combined with other pharmacologic activators to study the epistatic crelationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be controduced into any tumour cell (primary or cultured), and peptides cidentified which by themselves induce apoptosis, cell death, loss of cell cidentified which by themselves induce apoptosis, cell death, loss of cell cidentified which by themselves induce apoptosis, cell death, loss of cell cidentified which by themselves induce apoptosis, cell death, loss of cell constitutive function of the broactive peptides which restore the constitutive function of the broactive peptides which restore the constitutive function cell important in breast cancer such as the adenomatous polyposis coli gene cell-cell junctions, neurobiology applications, bone biology applications, skin cell-cell junctions, infectious disease applications, bone biology applications, skin biology applications, and allergic response applications, immunobiology, inflammation, and allergic response applications, and bibracies and drug response applications, and bibracies and drug cell such calls and cultivated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such constitutions. The meth
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Best Local S
Matches 16
                                                                                                                                                                                     Sequence 75
                                                                                                                                                                                                                                      restricted form.
                                                                                             16;
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AAAAEAAAKAAAEAAAKAAAEAA
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                                                                                                                                                                                        B
                                                                                             Conservative
                                                                                                              58.1%;
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    27
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                                                                                                                                      Length 75;
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Search completed: April 20, Job time : 56 secs 2004, 21:59:10

The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence;

Disclosure;

SEQ ID

NO 103; 110pp;

English

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Total number of hits satisfying chosen parameters:
                                           Searched:
                                                                              Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                            Sequence:
                                       .389414 seqs, 51625971 residues
                                                                                                                                                              US-10-019-482-1
105
                                                                                                                                                                                                                      April 20, 2004, 21:58:10; Search time 23 Seconds (without alignments) 56.115 Million cell updates/sec
                                                                                                                                          1 AXAEAAEKAAKYAAEAAEKAAKAXA 25
                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
    389414
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
×	60	57.1	33	-	US-08-303-025-16	Sequence 16, Appl
2		57.1	33	N	-08-436-703B-	e 4
3		•	56	4.	-09-405-	ω
4.	59	•	469	4.	-489-	139
₅	7.	•	67	4.	-09-869-875-7	7
თ	7.	•	86	4.	-09-	٠ م
7	57.5	•	117	4	US-09-340-736E-9	9
80	7	•	118	4	US-09-340-736E-10	10,
9	7.	•	199	4	- 1	11,
10	.7	•	200	4	US-09-340-736E-2	2, Appl
11	7.	٠	201	N	US-08-911-364-2	2
12	57.5	54.8	731	N	US-08-911-364-1	1, Appl
13	7	•	731	4	US-09-340-736E-1	1, Appl
14	7.	•	733	w	US-08-464-700-2	2
15	56	53.3	45	4.	US-09-405-743A-2	2, Appl
16	56	53.3	92	4	US-09-344-529-2	2, Appl
17	56	•	109	4	US-09-405-743A-7	7,
18	55	•	28	μ	US-08-303-025-12	12
19	55	52.4	28	N	US-08-436-703B-1	Sequence 1, Appli
20	55	52.4	29	ب	US-08-152-488-10	10,
21	55	52.4	29	_	US-08-152-488-11	11,
22	55	52.4	29	_	-488-1	e 12,
23	55	52.4	29	Ь	03-025-1	
24	55	52.4	29	Н	03-	e 11,
25	55	52.4	29	_	-025-	13,
26	55	52.4	29	ш	US-08-303-025-14	Sequence 14, Appl
27	55	52.4	29	ب	US-08-677-304-10	10,

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49.5	50	50.5	50.5	52	52	52	53.5	54	55	55	55	55	55	ភូ	55	55	55
47.1	47.6	48.1	48.1	49.5	49.5	49.5	51.0	51.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4
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US-09-117-121-28	US-09-117-121-30	US-08-858-207A-312	US-08-491-527A-13	US-09-252-991A-29581	US-09-117-121-38	US-09-117-121-37	US-09-405-743A-4	US-09-405-743A-5	US-08-436-703B-2	US-08-677-304-13	US-08-303-025-15	US-08-152-488-13	US-08-436-703B-16	US-08-436-703B-15	US-08-436-703B-3	US-08-677-304-12	US-08-677-304-11
Sequence 28, Appl	Sequence 30, Appl	Sequence 312, App	Sequence 13, Appl	Sequence 29581, A	Sequence 38, Appl	Sequence 37, Appl	Sequence 4, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 13, Appl	Sequence 15, Appl	•	Sequence 16, Appl		Sequence 3, Appli	Sequence 12, Appl	Sequence 11, Appl

ALIGNMENTS

RESULT 1

INFOR	PRI		US-08-303- Sequence Patent N GENERAL APPLI
TELEPIONE: 313-4: INFORMATION FOR SEQ SEQUENCE CHARACTEE LENGTH: 33 amin TYPE: amino ac: STRANDEDNESS: 1 TOPOLOGY: N/A MOLECULE TYPE: p ORIGINAL SOURCE: ORIGIN	CURKEN! APPLICATION UMM PILING DATE: 01 CLASSIFICATION: CLASSIFICATION PRIOR APPLICATION UMM APPLICATION UMM FILING DATE: 11 APPLICATION UMM REFERENCE/DOCKET REFERENCE/DOCKET	CORRESPONDENCE ADJUSTED TO SERVICE TO STREET: 150 We CITY: Detroit STATE: Michigal COUNTRY: United COUNTRY: UN	US-08-303-025-16 ; Sequence 16, Appli ; Patent No. 5614494 ; GENERAL INFORMATI ; APPLICANT: Wak APPLICANT: Sta ; APPLICANT: Sta ; TITLE OF INVENT ; TITLE OF INVENT ; TITLE OF INVENT ; TITLE OF INVENT
		CORRESPONDENCE ADDRESS: ADDRESSEE: Benita J, STREET: 150 West Jeff CITY: Detroit STATE: Michigan COUNTRY: United State COUNTRY: United State COUNTRY: United State COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER: IBM PC comp OPERATING SYSTEM: MS- SOFTMARE: WORDPEFECT	cation ON: ON: efield rews, nley, nloN: ION: ION:
6-7622 8454 805 16: NO: 16: Acids acids	US/08 -1994 -1994 PCT/U PCT/U 1992 US 08 US 08 1993 ION:	0.00 40	US/08303025 Thomas W. phillp C. James C. NOVEL PEPTIDES FOR HEPARIN A NOVEL PEPTIDES FOR HEPARIN A NOTICOAGULATION REVERSAL
	US/08/303,025 US/08/303,025 L1994 PCT/US92/06829 1992 US 08/152,488 11993 TON: RE: 7WH-060548-00231	Suite: erica erica 3.5"	W. W. TIDES FOULAR WEIGHARION R
	-00231	2500 1.44Mb (DOS) Text	FOR HEPARIN WEIGHT HEPAR
			IN DUX

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; TITLE: N/A; DOCUMENT NUMBER: PCT/US92/08069; FILING DATE: 14-AUG-1993
US-08-303-025-16
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US-08-436-703B-4
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                                                               US-08-436-703B-4
                                                                                                                                                                                                          TELEFAX: 313-905 - 4:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 33 amino acids
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Best Local (
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               Query Match
Best Local S
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 Matches
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APPLICANT: Wakefic
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIDIM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
                                                                                                            PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 313-965-1976
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                      JBLICAL
AUTHORS: N/A
 Local Similarity nes 14; Conserv
                                                                                                                                                                                                                                                                                                                         NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7W
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                                                                                                                             ORGANISM: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Detroit
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                                                                                                                                                                              TOPOLOGY:
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STREET: 6601 Woodward Avenue
                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanley, James C.
VENTION: NOVEL PEPTIDES FOR
VENTION: HEPARIN AND LOW MOLECULAR
VENTION: WEIGHT HEPARIN
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70.0%;
57.1%; Score 60; DB 2; Length 33; 70.0%; Pred. No. 0.026; tive 3; Mismatches 3; Indels
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Pred. No. 0.026;
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                                                                                                                 US-09-869-875-7
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                                                                                                                                RESULT 5
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LENGTH: 56
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13565
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 65.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Yeda Re
                                                                              Sequence 7, Application US/09869875 Patent No. 6521456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13565, Application US/09489039A Patent No. 6610836
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                                                                  GENERAL INFORMATION:
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APPLICANT: Siebenkotten, Gregor
APPLICANT: Christine, Rainer
TITLB OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC AC
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                LENGTH: 46
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                  302 AAAAEKAAAAEKAAADKAAKAAA 324
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                                                                                                                                                                                                                                                                                                                                                                   469
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                                                                                                                                                                                                                                                                 56.2%;
                                                                                                                                                                                                                                                Score 59; DB 4;
Pred. No. 0.7;
1; Mismatches
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Pred. No. 0
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CURRENT APPLICATION NUMBER: US/09/869,875
CURRENT APPLICATION NUMBER: US/09/869,875
CURRENT FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-01-03
PRIOR PHILOR DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
PRIOR PHILOR DATE: 1999-01-09
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 15
SOFTMARE: Patentin version 3.1
                                                                                                                                                                                                                       Sequence 9, Application US/09340736E Patent No. 6489446
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LENGTH: 86
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Best Local :
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APPLICANT: KOTHSTEIN, ASER
APPLICANT: KCHELEY, FRED
APPLICANT: KCHELEY, FRED
APPLICANT: ROTHSTEIN, STEVEN
APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR APPLICATION NUMBER: 08/911,364
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CURRENT FILING DATE: 199-09-24
NUMBER OF SEQ ID NOS: 7
SOPTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
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ORGANISM: Artificial Sequence
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Pred. No. 0.17
1; Mismatches
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US-09-340-736E-11
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US-09-340-736E-9
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                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                          Sequence 11, Application US/09340736E
Patent No. 6489446
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Patent No. 6489446
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Best Local Similarity
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Best Local Similarity
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        APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELEY, FRED
APPLICANT: KEELEY, FRED
APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0110
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0110
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SOFTWARE: PatentIn Ver. |2.1
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ORGANISM: Artificial Sequence
PEATURE:
PRIOR APPLICATION NUMBER: 08/911,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: MFU-4 polypeptide
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Pred. No. 0.
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Pred. No. 0.
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LENGTH: 199
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LENGTH: 200
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Best Local Similarity
Matches 17; Conserv
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Patent No. 5969106
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APPLICANT: KEELEY, FRED
APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 199-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
PRIOR FILING DATE: 1996-08-07
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PRIOR FILING DATE: 1996-08-07
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PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
                                                           GENERAL INFORMATION:
APPLICANT: KOTHSTEIN, Aser
APPLICANT: KEELY, Fred W.
APPLICANT: KEELY, Fred W.
APPLICANT: ROTHSTEIN, Steven J.
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Artificial Sequence
FEATURE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                          NUMBER OF SEQUENCES:
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; MOLECULE TYPE: peptide
US-08-911-364-2
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Patent No. 59691
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APPLICATION NUMBER: US 60/023,552
APPLICATION NUMB
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TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                           COUNTRY: U.S.A.

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                          APPLICATION NUMBER: US/08/911,364
FILING DATE: 07-AUG-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/023,552
FILING DATE: 07-AUG-1996
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CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 AQAAAAAKAAKYGVGTPAAAAAKAAKA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservation 54.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROTHSTEIN, Steven J.
VENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROTHSTEIN, Aser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEELY, Fred W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOLEY & LARDNER
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Pred. No. 0.44
1; Mismatches
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REGISTRATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                     Sequence 2, Application US/08464700 Patent No. 6232458
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR APPLICATION NUMBER: 08/911,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELEY, FRED
APPLICANT: KEELEY, FRED
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1996-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 731
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REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1070-5300
                                                                           APPLICANT: WEISS, ANTHONY S
APPLICANT: MARTIN, STEPHEN I.
TITLE OF INVENTION: SYNTHETIC
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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COUNTRY:
                                             STREET:
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TOPOLOGY: linear
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                                                                   DDRESSEE:
                                                                                                                                                                                                                                                                                                  415 AQAAAAAKAAKYGVGTPAAAAAKAAAKA 442
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            Spring House Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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17; Conservative
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                                               Spring House Corporate Cntr,
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                  Howson and Howson
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                                                                                                                     SYNTHETIC POLYNUCLEOTIDES
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    Mismatches

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Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09405743A

Patent No. 6514938

GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                   Query Match
Best Local Similarity 60:9
                                                                                                                                                                                                               SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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APPLICATION NUMBER: AU PL6520
FILING DATE: 22-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL9661
PILING DATE: 28-JUN-1993
PRIOR APPLICATION DATA:
PCT/AU93/00655
PILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION TO DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00655
PILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                  FEATURE:
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CUBRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 54.8%;
Local Similarity 60.7%;
nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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19 AAEAKKAAKYEKAAAEKAAAKEA 41
                                  3 АЕАЛЕКЛАКУАЛЕАЛЕКАЛКАХА 25
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                                                                                     53.3%;
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Pred. No. 1.9;
1; Mismatches
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Pred. No. 0.14;
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                                                                                                        Length 45;
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Search completed: April 20, 2004, 22:01:34 Job time : 23 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2 / f/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2-6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/USO6 PUBCOMB.pep:*

5: /cgn2-6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

6: /cgn2-6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2-6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

7: /cgn2-6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

7: /cgn2-6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
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105
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/Ggn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
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6/ptodata/1/pubpaa/US09A
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	- ;	•													
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Score	65	65	65	65	62.5	62	62	62	62	62	62	62	62	61.5	7
Query Match I	61.9	61.9	61.9	61.9	59.5	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	58.6	מת
Length	104	104	104	104	428	104	104	104	104	104	104	104	104	104	104
ם ו	12	12	14	14	12	12	12	12	12	14	14	14	14	12	3
ID	US-10-393-449-42	US-10-393-449-92	US-10-177-725-42	US-10-177-725-92	US-10-282-122A-55748	US-10-393-449-39	US-10-393-449-40 ·	US-10-393-449-89	US-10-393-449-90	US-10-177-725-39	US-10-177-725-40	US-10-177-725-89	US-10-177-725-90	US-10-393-449-41	TC_10_303_440_01
Description	Sequence 4		Sequence 4			Sequence 3	Sequence 4	Sequence 8	Sequence 9	Sequence 3	Sequence 4	Sequence 6	Sequence 9	Sequence 4	Semience
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	App	ģ	aga	Appl	۳	ģ	gg.	App	ģ	ģ	ģ	ģ	ģ	g	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓

ALIGNMENTS

RESULT 1 US-10-393-449-42

Qy Db	Query	; FEA ; OTH US-10-3	ORG	SEQ I	; NUMB	; PRIO	PRIO	; PRIO	; PRIO	· · · CURIR	; FILE	; APPL	; APPL	; APPL	GENER	; Seque	
MATCHES 17; CONSETVATIVE 0; MISMATCHES 8; INCEIS 0; GADS 0; 2y	atch 61.9%; Score 65; DB 12; Length 104; cal Similarity 68.0%; Pred. No. 0.12;	; FEATURE: ; OTHER INFORMATION: synthetic US-10-393-449-42	TYPE: PRT ORGANISM: Artificial sequence	SEQ ID NO 42	; NUMBER OF SEQ ID NOS: 173 ; SOFTWARE: PatentIn version 3.1	; PRIOR FILING DATE: 1998:10-08	PRIOR FILING DATE: 1999-10-08	; PRIOR FILING DATE: 2002;06-20 ; PRIOR APPLICATION NUMBER: US 09/415,765	PRIOR APPLICATION NUMBER: US 10/177,725	CURRENT APPLICATION NUMBER: US/10/393,449	; FILE REFERENCE: RIGU-007CIP3	; APPLICANT: Peele, Beau R.	; APPLICANT: Bogenberger, Jakob M.	APPLICANT: Anderson, David	GRANDAL INFORMATION:	. Biblication No IngonanceAdlean	
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RESULT 2

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CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 92
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Publication No. US20030224412A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: RIGL-007CIP3
                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
EQ ID NO 42
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, David APPLICANT: Bogenberger, Ja
                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
                                                                                      ORGANISM: Artificial sequence FEATURE:
                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC FEATURE LOCATION: (37)...(68)
COCATION: (37)...(68)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, 53-54, 56-58, OTHER INFORMATION: 2, 64-65, and 67-69 can be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (37)..(68)
OTHER INFORMATION: "Xaa" at
OTHER INFORMATION: 1, 63-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial sequence
                                                                OTHER INFORMATION: synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
17; Conser
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Peele, Beau R.
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Peele, Beau R.
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llarity 68.0%;
Conservative
61.9%;
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Score 65;
DB 14; Length 104;
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US-10-282-122A-55748
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Matches 17; Conservative
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Publication No. US20040029129A1
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Best Local
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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT E
FILE REFERENCE: A-66900-4/RMS/AMS
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CURRENT APPLICATION NUMBER: US/10/282,122A
                    FILE REFERENCE: ELITRA.034A
                                                                                                                  APPLICANT:
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TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, OTHER INFORMATION: 2, 64-65, and 67-69 can be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE LOCATION: (37)...(68) LOCATION: (37)...(68) CTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
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OTHER INFORMATION: synthetic
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                        INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 АХАЕААЕКААКҮААЕААЕКААКАХА 25
                                                                                                                                                                                                                            : Wang, Lianger
: Zamudio, Carlo
: Malone, Cheryl
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                                                                                                                                      Trawick, John
                                                                                                                                                                         Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                  Haselbeck,
                                                                       Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                              Grant
                                                                                                                                                       Danie
                                                                                                                                                                                                                                                        Carlos
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Pred. No. 0.12;
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CURRENT FILING DATE:

2003-02-20

60/191,078

APPLICATION NUMBER:

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                                                                                                                                       ; OTHER INFORMATION: synthetic US-10-393-449-39
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
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                                                                              Query Match
Best Local
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SEQ ID NO 39
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, David
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                                                                                                                                                                           FEATURE:
                                                                                                                                                                                           ORGANISM: Artificial sequence
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1 AXAEAAEKAAKYAAEAAEKAAKAXA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AXAEAAEKAA-----KYAAEAAEKAAKA 23
                                                                              Similarity
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Peele, Beau R.
                                                            Conservative
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Pred. No. 1.
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RESULT 8
US-10-393-449-89
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; OTHER INFORMATION: synthetic US-10-393-449-40
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SOFTWARE: Patentin version 3.1
SEQ ID NO 89
LENGTH: 104
TYPE: PRT
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Publication No.
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LENGTH: 104
TYPE: PRT
ORGANISM: Artificial sequence
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Best Local (
PEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (37). (68)
OTHER INFORMATION: "Xaa"
OTHER INFORMATION: 1, 63
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Publication No.
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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CURRENT APPLICATION NUMBER: US/10/393,449
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APPLICANT: Beele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, David
APPLICANT: Bogenberger, J
APPLICANT: Peele, Beau R.
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CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                   ORGANISM: Artificial sequence FEATURE:
                                                                                                          OTHER INFORMATION: synthetic
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No. US20030224412A1
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  "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 1, 63-64 and 66-68 can be any amino acid
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Pred. No.
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                                                         SEQ ID NO 39
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CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
                                                                                                                                                                                           TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RNS/AMS CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
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                                                                       NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
                                                                                                              PRIOR APPLICATION NUMBER: US 09/169,015 PRIOR FILING DATE: 1998-10-08
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OTHER INFORMATION: "X.
OTHER INFORMATION: 1,
ORGANISM: Artificial sequence
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OTHER INFORMATION: synthetic
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ORGANISM: Artificial sequence
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Peele, Beau R.
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Peele, Beau R.
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Pred. No. 0.29;
0; Mismatches
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Pred. No. 0.29
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; FEATURE:
; OTHER INFORMATION: synthetic US-10-177-725-39
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SEQ ID NO 40
LENGTH: 104
                                                                                             SEQ ID NO 89
LENGTH: 10
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Best Local &
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Publication No.
                                                                                                                                                                     FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
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APPLICANT: Bogenberger, J
APPLICANT: Peele, Beau R.
                                                                                                                                    SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2002-06-20
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
                                                                                                                                                                                                                                                                                                                  APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
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          FEATURE:
OTHER INFORMATION: synthetic
                                                   ORGANISM: Artificial sequence
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FEATURE:
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Similarity 72.0%;
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No. US20030143562A1
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No. US20030143562A1
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Pred. No. 0.29
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Sequence 41, Application US/10393449
Publication No. US20030224412A1
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Hogenberger, Jakob M.
APPLICANT: Begenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT APPLICATION NUMBER: US 10/177,725
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR PEPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/4169,015
PRIOR APPLICATION NUMBER: US 09/169,015
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SOFTWARE: PatentIn version
SEQ ID NO 90
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Best Local Similarity
Matches 18; Conserv
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CURRENT FILING DATE: 2002-06-20
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PRIOR FILING DATE: 1998-10-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
LOCATION: (37)..(68)
OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57,
OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
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Peele, Beau R.
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No. US20030143562A1
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Search completed: April 20, Job time : 43 secs
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2003-03-18
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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NAME/KEY: MISC_FEATURE
LOCATION: (37)...(68)
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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No. US20030224412A1
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72.0%;
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Pred. No. 0
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Database :
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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PIR 78:*
1: pir1:*
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105
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 AXAEAAEKAAKYAAEAAEKAAKA 23 | |:||||| : || ||:||| |

ALIGNMENTS

hypothetical protein 720K18 130 - Arabidopsis thaliana ()Species: Arabidopsis thaliana (mouse-ear cress) ()Species: Apr.1999 fleequence _revision 23-Apr.1999 flext_change 22-Oct-1999 ()Accession: 706636 ()Risevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mer submitted to the Protein Sequence Database, April 1999 ()A; Argerimental source: cultivar Columbia; BAC clone T20K18 ()A; Arabidopsis thaliani source: cultivar Columbia; BAC clone T20K18 ()A; A; A	RESULT 1 T06636 hypothetical protein T20K18.130 - Arabidopsis thaliana
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C;Species: Es
C;Date: 07-Se
C;Accession:
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
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F97683
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AF2908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Genome Sequence of the Plant Patho A; Reference number: A97359; MUID: 21608551;
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  tolA protein - Escherichia coli (strain K-12) (;Species: Escherichia coli (C;Date: 07-Sep-1990 #sequence_revision 07-Sep (C;Accession: JV0057; B64810
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE007869; PIDN:AAK88423.1; PID:g15157917; GSPDB:GN00169
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                                                                                                                                                                                                                                                                                                                         ;Map position: circular chromosome
;Superfamily: Escherichia coli ribosomal protein L19
                                                                                                                                                                                                                                                                                                                                                                Gene: AGR_C_4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: F97683
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Species: Agrobacterium tumefaciens
;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
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Species: Agrobacterium tumefaciens
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Best Local
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                                                                                                                                                                                                        AXAEAAEKAAKYAAE--AAEKAAKA 23
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                                                                                                                                                                AQALAAEKAAAEAAEAKAAEEAAKA
                                                                                                                                                                                                                                              57.1%;
llarity 72.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the Plant Pathogen and Biotechnology 59; MUID:21608551; PMID:11743194
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Pred. No. 1.6;
1; Mismatches
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                      07-Sep-1990
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                  #text_change
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Markelz,
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rkelz, B.;
    genome polyprotein 1 - tomato ringspot virus
C;Species: tomato ringspot virus
                                             GNVVSR
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                                                                RESULT
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u. Bacteriol. 171, 6600-6609, 1989
A,Title: Nucleotide sequences of the tolA and tolB genes A,Reference number: JV0057; MUID:90078104; PMID:2687247
A,Accession: JV0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: the authors translated the initiation codon GTG for residue 1 as Val R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                               R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: nucleotide binding; P-loop; transmembrane protein F;14-34/Domain: transmembrane #status predicted <MSS> F;78-301/Domain: helical #status predicted <HSR> F;355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960.
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-421 <BLAT>
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A; Residues: 1-421 < LEV >
                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Start codon:
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                                                                                                                                                                                                                                                                                                                    A;Reference number: A87249; MUID:21173698; A;Accession: E87294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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                                             AXAEAAEKAAKYAAEAAEKAAKAXA 25
ASAEAAERQAKEEAVLAEKLAAAEA
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                                                                                        Conservative
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                                                                                                              54.3%;
                                                                                        Score 57; DB Pred. No. 3.7; Mismatches
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Pred. No.
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(strain

raspberry)

(fragment)

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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2328
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PFB0035c
C;Superfamily: Plasmodium falciparum rifin PFB1005w
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A;Title: Comparison of the 5' and 3' termini of tomato ringspot virus RNA1 and A;Reference number: A40787; MUID:92024112; PMID:1926788
A;Accession: A40787
                   A; Residues: 1-564 < KUR>
A; Cross-references: GB:
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A;Experimental source: clone 3D7
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A; Residues: 1-375 < GAR >
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                                                                    A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: M73822; NID: g335267; PIDN: AAA47941.1;
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A; Residues: 1-354 < ROT>
                                                                                                                                                                                                                                                                                                                                                  ATP-binding protein of ABC transporter all4183 [imported] - Nostoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ifin PFB0035c - malaria parasite (Plasmodium falciparum)
;Species: Plasmodium falciparum
;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 02-Mar-2001
;Accession: A71625
  Cross-references: GB:BA000019; PIDN:BAB75882.1; PID:g17133318; Experimental source: strain PCC 7120
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                                                                                         Status: preliminary
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Pred. No. 9.
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RESULT 12
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A;Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32376.1; PID:g4894288
A;Experimental source: strain Sterne
A;Note: similar to hypothetical, locus Clo tetP Clostridium perfringens (L20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein pXO1-72 - Bacillus anthracis virulence plasmid pXO1 C;Species: Bacillus anthracis C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbor
A;Reference number: A59091; MUID:99445483; PMID:10515943
A;Accession: H59099
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A;Residues: 1-909 <BEV>
A;Cross-references: EMBL:AL049640; GSPDB:GN00062; ATSP:T20K18.120
A;Experimental source: cultivar Columbia; BAC clone T20K18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T20K18.120 - Arabidopsis thali
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999
                                                                                                                                                                                                A;Gene: pX01-72
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-101 <0
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                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: H59099
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A;Introns: 205/2; 686/3; 740/3; 772/2; 808/3; 838/3; 897/3
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A;Accession: T06635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; submitted to the Protein Sequence Database, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
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                                                                                                                                                            Superfamily: Bacillus anthracis virulence plasmid pXO1 hypothetical
                                                                                                                    Query Match
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44 AEEKAAEKAAKEAAEEARIATK 65
                                    1 АХАЕААЕКААКҮААЕААЕКААК 22
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Pred. No.
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Pred. No. 25;
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C;Species: Citrobacter freundii
C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: 140794; A03504; I40777
C;Accession: 140794; A03504; I40777
R;Morlon, J.; Chartier, M.; Bidaud, M.; Lazdunski, C.
Mol. Genet. 211, 231-243, 1398
Mol. Genet. 211, 231-243, 1398
A;Title: The complete nucleotide sequence of the colicinogenic plasmid ColA. High extent
A;Reference number: 140778; MUID:88174422; PMID:2832701
                                                                                                                                                                                                                                                                                                                                       R;Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L. Eur. J. Biochem. 168, 629-633, 1987
A;Title: Structural variations in the alanine-rich antifreeze A;Reference number: S02376; MUID:88029483; PMID:3665937
A;Accession: S02376
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C;Superfamily: colicin IB
C;Keywords: antibiotic; bacteriocin; toxin; transmembrane protein
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A;Residues: 1-53, YX, 55-70 <RE2>
A;Residues: 1-58, YX, 55-70 <RE2>
A;Cross-references: GB:M26369; NID:g144659; PIDN:AAA98057.1; PID:g144660
A;Experimental source: plasmid Cola
C;Comment: This protein acts to depolarize the bacterial inner membrane,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antifreeze protein precursor - yellowtail flounder C;Species: Limanda ferruginea (yellowtail flounder) C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989
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S02376
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                                                                                                                                                                                                       A;Cross-references: EMBL:X06356; NID:g64041; PIDN:CAA29655.1; A;Note: part of this sequence, including the amino end of the C;Superfamily: antifreeze protein
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A; Residues: 1-97 <SCO>
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A;Residues: 1-592 <MOR>
                                                                                               ;Keywords: antifreeze;1-23/Domain: signal sequence #status predicted <SIG>;1-23/Domain: propeptide #status predicted <PRO>;24-48/Domain: propeptide #status predicted <PRO>;49-96/Product: antifreeze protein #status predicted
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Search completed: April 20, Job time : 22 secs

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A;Residues: 1-394 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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gasawara, N.; Yasunaga, T.; Kuhara, S.;
DNA Res. 8, 11-22, 2001
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                                                                                                                                                                                                                                                                                 A; Reference number: A85480; A; Accession: G85576
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A;Experimental source: strain O157:H7, substrain EDL933
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A; Residues: 1-394 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
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                                                                                                                                 A;Gene:
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A;Reference number: A85480; MUID:21074935; PMID:11206551
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P19934;
                                                                         Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                       Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K. Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.,
                                                                                                                                                                                                                                                                               MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., May
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rc
Mau B., Shao Y.;
          MEDLINE=91296736; PubMed=2068069; Levengood S.K., Beyer W.F. Jr., Webster R.E.; "Tolh: a membrane protein involved in colicin uptake extended helical region.";
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Levengood S.K., Webster R.E.;
"Nucleotide sequences of the tolA and tolB genes and localization their products, components of a multistep translocation system in
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JM105;
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PIR; F97683; F97683
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                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 171:6600-6609(1989)
                                                                                                                                                                                                                                                      complete genome sequence of Escherichia coli K-12.", nce 277:1453-1474 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with its coreceptor, the C-terminal Structure 7:711-722(1999).
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MEDLINE=99332679; PubMed=10404600;
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-i- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
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EcoGene; EG11007; tolA.
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DOMAIN II (ALPHA-HELICAL).

DOMAIN III (FUNCTIONAL).

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01-APR-1990
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Elastin prec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM B).

MEDILINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P.,
Rosenbloom J.C., Peltonen L., Rosenbloom J.;

Rosenbloom J.C., Peltonen L., Rosenbloom J.;

"Alternative splicing of human elastin mRNA indicated analysis of cloned genomic and complementary DNA.";

Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        odelberg S.J., Keating M.T.;
"LIM-kinasel hemizygosity implicated constructive cognition.";
Cell 86:59-69(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hippocampus, and Placenta; MEDLINE=96291399; PubMed=8689688; Frangiskakis J.M., Ewart A.K., Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fazio M.J., Olsen D.R., Kuivanie
Rosenbloom J., Uitto J.,
"Isolation and characterization
associated variation in elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J., Robinson B.F., Klein B.P., Ensing G.J., Eve Green E.D., Proeschel C., Gutowski N.J., Noble M., Atkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P15502; Q14;
01-APR-1990
                                                                                between
                                                                                                       This SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 603-730 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88156138; PubMed=2831431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 164-724 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
             s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Major structural protein of tissues nuchal ligament, which must expand rapidly and SUBUNIT: The polymeric elastin chains are crossinto an extensible 3D network.

SUBCELLULAR LOCATION: Extracellular matrix of ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                               IsoId=P15502-2; Sequence=VSP 004243; PTM: The crosslinks are made of deaminated Lys. DISEASE: Haploinsufficiency of ELN may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in many better than the control of the 
                                                                                                                                                      Williams-Beuren syndrome (WBS), a rare is a contiguous gene deletion syndrome chromosome band 7q11.23.
                                                                                                                                                                                                                                                                                                                                                    Name=2
                                                                                                                                                                                                                                                                                                                                                                                                         Name=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Invest.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Comment=Additional isoforms
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1990 (Rel. 14, Last sequence update)
2003 (Rel. 42, Last annotation update)
precursor (Tropoelastin).
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J., Uitto J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibroblast;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of human elastin cDNAs, and age-
gene expression in cultured skin
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                                                                                                                                                                               normalities observed in developmental disorder. involving genes from
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M., Atkinson D.
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MIM; 130160;
MIM; 130160;
MIM; 194050;
GO; GO:000551
GO; GO:000520
GO; GO:000828
GO; GO:0000739
GO; GO:000739
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         SEQUENCE FROM N.A. MEDLINE=92024112; Po Rott M.B., Tremaine
                                                              RNA1 polyprotein (Fragment).
Tomato ringspot virus (isolate
Viruses; ssRNA positive-strand
                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X15603;
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                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                             GO; GO:0007585; P:respiratory gaseous InterPro; IPR003979; tropoelastin. PRINTS; PR01500; TROPOELASTIN.
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HSSP; P50099; 1ZFJ.
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                                           NCBI_TaxID=12281;
                                                                                                                                                                                                                                                                                                                                                       GO:0005578; C:extracellular matrix; TAS.
GO:0005615; C:extracellular space; TAS.
GO:0005201; F:extracellular matrix structural constituent;
GO:0008283; P:cell proliferation; TAS.
GO:0008015; P:circulation; TAS.
GO:0007397; P:histogenesis and organogenesis; TAS.
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M36860;
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17; Conserv
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                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                           syndrome;
 pubMed=1926788;
ne J!H., Rochon D.M
e 5' and 3' termini
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Pred. No. 4.1;
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/FTId=VSP_004243.
; AB06D15BA567AE46 CRC64;
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BY SIMILARITY
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                                                               raspberry) (TomRSV).
viruses, no DNA stag
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tomato ringspot virus
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RC STRAIN-Berkeley;

WMEDLINE=20196006; PubMed=10731112;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams M.D., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

RA Henderson S.H., Farandale J., Balang Q., Chen L.X.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Man K.H., Doyle C., Baxter B.P., Bandari D., Baldwin D.,

Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ra Baltis K.C., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleisehmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleisehmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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EMBL; M73822; AAA47942.1; A
PIR; A40787; GNVVSR.
Polyprotein; Coat protein.
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Q9VGX3; Q95S18; Q9VGX1; Q9VGX2; Q9Y0F9;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology 185:468-472(1991).

-i- SIMILARITY: IDENTICAL FOR THE FIRST 132 AA, AND FOR THE NEXT 145 AA TO THE RNA2 POLYPROTEIN.

-i- CAUTION: It is uncertain whether Met-1 or Met-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99097004; PubMed=9878744;
Ma E., Xu T., Haddad G.G.;
"Gene regulation by O2 deprivation: an anoxia-regulated novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anoxia upregulated protein. FAU OR CG6544.
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
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RA Harris N.L., Harvey D.A., Heiman T.J., Wein.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lisko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers B.M., Rubin G.M., Venter J.C.;
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Rubin G.M., Celniker S.E.;
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Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
Genome Diol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Berkeley; TISSUE-Head;
MEDLINE-22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.B., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, AND ALTERNATIVE SPLICING. MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                      This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Carlson J.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Annotation of the Drosophila melanogaster euchromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Plays an important role in responsiveness to oxygen deprivation. ALTERNATIVE PRODUCTS:
                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                TISSUE SPECIFICITY:
                                                                                                                                                                                          INDUCTION: BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing; Named isoforms=5; Comment=Experimental confirmation may be lacking
                                                                                                                                                                                                                                                                                         IsoId=Q9VGX3-4;
                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9VGX3-2;
                                                                                                                                                                                                                                                   IsoId=Q9VGX3-5;
                                                                                                                                                                                                                                                                                                                           IsoId=Q9VGX3-3; Sequence=VSP_004046,
                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9VGX3-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             isoforms;
                                                                                                                                                                                                        UB SPECIFICITY: Concentrated in lamina neurons, neurons and cortical neurons of central brain.
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Y: Concentrated in la
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b J.M., Park S.,
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MEDLINE-84036205; PubMed=6313941;

MORION J., Lloubes R., Varenne S., Cha-
MORION J., Lloubes R., Varenne S., Cha-
"Complete nucleotide sequence of the s
gene translated at non-uniform rate.";
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J. Mol. Biol. 224:639;657(1992).

-I- FUNCTION: This colicin is a channel-forming colicin. This creates the cytoplasmic membrane transmembrane toxins depolarize the cytoplasmic membrane, to dissipation of cellular energy.

-I- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND CLOSELY RELATED BACTERIA.
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PDB; 1COL; 15-JUL-93.
InterPro; IPR000293; Channel_colicin.
Pfam; PF01024; Colicin; 1.
                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                               PRINTS; PR00280; CHANICOLICIN.
PRODOM; PD002657; Channel_colicin; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
Antibiotic; Bacteriocin; Plasmid; Transmembrane; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                              modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Refined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92235820; PubMed=1373773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMED outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on J., Chartier M., Bidaua m., on J., Chartier M., Bidaua m., on J., Chartier M., Bidaua m., complete nucleotide sequence of t complete nucleotide sequence of t extent of homology with ColBi.";
 364
                                                                                                                                                                                                                                                                                                                                                                                             X01008; CAA25503.1;
M37402; AAA72879.1;
                                      Similarity
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AAAEAAEKARQRQAEEAERQRQA 386
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                                                 Score 54;
Pred. No.
                                       Pred. No. 9.4
3; Mismatches
                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                             B80FA1F52A8CFC5D CRC64;
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domain of colicin
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colicinogenic plasmid ColA.
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P09031;
P09031;
P09031;
P09031;
O1-NOV-1988 (Rel. 09, Last sequence update)
O1-NOV-1988 (Rel. 09, Last sequence update)
O1-AUG-1990 (Rel. 15, Last annotation update)
Antifreeze protein precursor (AFP).
Limanda ferruginea (Yellowtail flounder).
Limanda ferruginea (Yellowtail flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectioidei; Pleuronectidae; Limanda.
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074225;
16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98225221; PubMed=9556627; Plesofsky-Vig N., Brambl R.; "Characterization of an 88-kDa heat shock protein of Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pe
Sordariomycetidae; Sordariales;
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InterPro; IPRO101023; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that interacts with Hsp30.";
J. Biol. Chem. 273:11335-11341(1998).
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                       Scott G.K., Davies P.L., Shears M.A., "Structural variations in the alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001
28-FEB-2003
                                                                      MEDLINE=88029483; PubMed=3665937;
                                                                                              SEQUENCE FROM N.A.
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SIMILARITY: Belongs to the heat shock protein 70 family.
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707 AA; 78673 MW;
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s; Sordariaceae;
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                       Fletcher G.L.; rich antifreeze
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Neurospora.
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                       proteins
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                                                                                                                                                                                                                                                                                      Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Wanalysis of the chromosome sequence of the legume symbiont sinorhizobium meilloit strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

-i FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyi-trna binding site (By similarity).
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50S ribosomal protein L19.
RPLS OR R03246 OR SMC03863.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
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                         EMBL; AL591793;
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S02376; S02376.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
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14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 АХАЕЛАЕКААКУАЛЕЛАЕКААКАХА
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                                                                                an email to license@isb-sib.ch).
                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41, Created)
(Rel. 41, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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BELONGS TO THE TYPE-I AFP FAMILY.
                           CAC47825.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53;
Pred. No.
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62AD582DF8E459B6 CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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TYPE 1 AFP ARE
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Best Local S
Matches 19
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                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Queen Anne's Lace;
MEDLINE=89384429; PubMed=2571069;
Franz G., Hatzopoulos P., Jones T.J.,
"Molecular and genetic analysis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Apiales; Apiaceae; Apioideae; Scandiceae; Daucinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAUCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGRO1024; rpls bact; 1.
PROSITE; PS01015; RIBOSOMĀL 119; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 177 AA; 19255 MW; 1BD19D
                                                                                                                                                                               Pfam; PF02987;
                                                                                                                                                                                                   PIR; S04909;
                                                                                                                                                                                                             EMBL; X16131; CAA34258.2;
                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: May play a role in late embryogeny.
-!- SUBCELLULAR LOCATION: Cytoplasmic, protein boo of zygotic embryo and endosperm tissue.
-!- SIMILARITY: Belongs to the LEA type 1 family.
                                                                                                                                                                                                                                                                                                                                                                    Daucus carota L.";
Mol. Gen. Genet. 218:143-151(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Embryonic protein DC-8.
                                                                                                                                                          DOMAIN
                                                                                                                                                                     Repeat
                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Daucus carota (Carrot).
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ProDom; PD002979; Ribosomal_L:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001857; Ribosomal_L19
Pfam; PF01245; Ribosomal_L19; T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQALAAEKAAAEAAEAKAAEEAKAAEAAA 176
                                                                                                                                                                                         IPR004238; LEA.
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Pred. No. 4.7;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                             in late embryogeny.
oblasmic, protein bodies,
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                                                                                                                                                          ×
                                                                                                                                                          APPROXIMATE TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                          Krauss M., embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                         gene,
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RESULT 12
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RESULT 11
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DT 01-AU
DT 01-BU
DT 15-JU
DT 01-BU
DT 15-JU
DT 10-AU
DR INTER
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Best Local S
Matches 13
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Best Local S
Matches 12
                                                                                                                                                                                                                                            PIR; A26721; A26721.

HSSP; P02259; 1HST.

InterPro; IPR005818; Histone H5.

InterPro; IPR005819; Histone H5.

InterPro; IPR005819; Linkerhist N.

Pfan; P700538; Histone; I.

PRINTS; PR00624; HISTONEH5,

ProDom; PD000373; Linkerhist N; 1.

SWART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P07796;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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SEQUENCE
                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=87172742; PubMed=3031476;
Knowles J.A., Lai Z.-C., Childs G.J.;
"Isolation, characterization, and exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Last annotation update)
Histone Hl-gamma, late.
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M16033; AAA30059:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purpuratus.";
Mol. Cell. Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus.
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                                                                                                                                                                                                                                 Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        late histone subtype Hl-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3chinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the histone H1/H5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Histones, H1 are necessary for the condensation nucleosome chains into higher order structures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 AEAKEKTGEYKDYAAQKAAEA 216
                                                 1 АХАЕААЕКААКҮААЕААЕКААКА 23
                                                                                                      13;
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12; Conserv
                                                                                                                              Similarity
AAAKPAKKAAKPAKKAAKPAKKA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                АЕААЕКААКУААЕААЕКААКА 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. 7:478-485 (1987).
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                                                                                                                                                                                                     217 AA; 22658
                                                                                                      Conservative
                                                                                                                                                                                                                            protein;
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                                                                                                                        49.5%;
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                                                                                                                                                                                                  Nuclear protein; DNA-binding; Multigene family.
22658 MW; C7251EED3413B185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.5%;
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                                                                                                 Pred. No. 7.3, 4; Mismatches
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                                                                                                                           Score 52; DB 1;
Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                   Length 217;
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                                                                                                   Gaps
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STANDARD;

PRT;

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RESULT 13
ANP8_MYOSC
ID ANP8_MYOSC
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Best Local :
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MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Saler M.H., Hancock R.E. M., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50600;
01-OCT-1996
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97113525; PubMed=8955385;
Dennis J.J., Lafontaine E.R., Sokol F.A.;
"Identification and characterization of the tolQRA genes
                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.";
J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
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Tola OR PA0971.
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                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                           Complete proteome.
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IIGRFAMs; TIGR01352; tonB_Ct
                                                                                                                                                                                                                                                                            PIR; E83525;
                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Involved
                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential).
                                                               171
                                                                                                                                                                                                                                                                                       U39558; AAC44660.2; -. AE004530; AAG04360.1;
                                                                                     -
                                                                                                                           Similarity
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                                                                                      AXAEAAEKAAKYAAEAAEKAAKAXA
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347
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(Rel.
(Rel.
                                                                                                                Conservative
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  STANDARD;
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347
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Last sequence update)
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brt; Transmembrane; Repeat; Inner
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                                                                                                             Score 52; DB
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                            POLY-ALA
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  PRT;
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11;
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                                                                                                                                       Length 347;
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nosa PAO1, a
                                                                                                                                                                                                                                                                                                                                                                                                                                         Inner membrane
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RESULT
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Best Local :
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Q8S339;
15-MAR-2004
15-MAR-2004
15-MAR-2004
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20-MAR-1987
20-MAR-1987
01-AUG-1990
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REPEAT
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20-MAR-1987 (Rel. 04, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
Antifreeze peptide SS-8.
Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).
Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei, Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hew C.-L., Joshi S., Wang N.-C., Kao M.H., Ananthanarayanan V.S., "Structures of shorthorn sculpin antifreeze polypeptides."; Bructures of shorthorn sculpin antifreeze polypeptides."; Biochem. 151:167-172(1985).

-i- FUNCTION: Antifreeze proteins lower the blood freezing point.

-i- SUNILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
                                                                                                                                                                                                                    plant Cell 14:2303-2314 (2002).

-|- FUNCTION: Required for the insertion of some light-harvesting complexes (LHC) proteins into the chloroplast thylakoid membrane. Essential for the assembly and activity of LHC I and II. Its function is probably partly distinct from that of ALB3.2.

-|- SUBUNIT: Associates with the LHCII complex and with the psaE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBU outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22204449; PubMed=12215522;
Bellafiore S., Ferris P., Naver H., Goo
"Logs of Albino3 leads to the specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., FUNCTION, SU WITH THE LHCII COMPLEX AND PSAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALB3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                  ight-harvesting system.";
                                                                                                                                                subunit of the LHCI complex. SUBCELLULAR LOCATION: Integr. thylakoid membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALANINE-RICH, A
, A05163; A05163
                                                                                                                        SIMILARITY: Belongs to the OXA1/oxaA family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 43, Created)
(Rel. 43, Last sequence update)
(Rel. 43, Last annotation updat
(Rel. 43, Last annotation toho
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                                                                                                                                                                          Integral membrane protein.
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Pred. No. 2
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L; Mismatches
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, chloroplast
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RESULT 15
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Best Local :
                                                                                                                                                                                                                                                                                     SEQUENCE FROM......

STRAIN=A3(2) / M145;

STRAIN=A3(2) / M145;

MEDIJINE=21996(10; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Cronin A., Fraser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Ruther S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Buter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger M., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger M., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger M., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger M., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger M., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger M., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
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Chloroplast; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
28-FEB-2003
10-OCT-2003
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
Nature 417:161-147(2002).

Nature 417:161-17:000 This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active -transport system. Enzyme I transfers the phosphoryl group from phosphoenolpyruvate (PEP) to the phosphoryl carrier protein (HPr).

Enzyme I is common to all PTS.
-I- CATALYTIC ACTIVITY: Phosphoenolpyruvate + protein L-histidine = pyruvate + protein N(pi)-phospho-L-histidine.
-I- SUBGULTULAR LOCATION: Cytoplasmic.
-I- SUBGELLULAR LOCATION: Cytoplasmic.
-I- SIMILARITY: Belongs to the PEP-utilizing enzyme family.
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Q9KZP1;
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TRANSMEM
DOMAIN
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phosphoemolpyruvate-protein phosphotransferase
(Phosphotransferase system, enzyme I).
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entities requires a license agreement (So
or send an email to license@isb-sib.ch).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomycineae; Streptomycetaceae; Streptomyces.
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INNER MEMBRANE ALBINO3-LIKE PROTEIN 1.
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Pred. No. 16;
3; Mismatches
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A9CDBF2C044AE37E CRC64;
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Search completed: April 20, Job time : 12 secs
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Matches 15
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HSSP; P22983; IDIK.
InterPro; IPR008731; PEP-utilisers N.
InterPro; IPR008279; PEP mobile.
InterPro; IPR006318; PEP trans.
InterPro; IPR006121; PEP_utilizers.
Pfan; PP0524; PEP-utilizers N; 1.
                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no will not be a subject of the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                          Pfam; PF00391; PED-utilizers; 1.
Pfam; PF02896; PEP-utilizers C; 1.
PF1NTS; PR01736; PHPHTENFRASE;
ProDom; PD000940; PEP utilizers; 2.
TIGRPAMS; TIGR01417; PTS I fam; 1.
PROSITE; PS00742; PEP ENZYMES PHOS SITE; 1.
PROSITE; PS00370; PEP_ENZYMES PHOS SITE; 1.
                                                                                                                                                                                                                                         Phosphotransferase system; Transferase; Kinase; Phosphorylation; Complete proteome.

ACT_SITE 186 186 TELE-HOSPHOHISTID1
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                                                                                             ААЕКААКУААЕААБ-КААКАХА 25
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57271
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               2004, 21:59:34
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PHOSPHORYLATION (BY SIMILARITY)
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Database
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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7: sp_mhc:*
8: sp_organelle:*
9: sp_blage:*
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202.255 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q9vgd2 drosophila	Q86bg1 drosophila	Q86pc3 drosophila	Q9w2j2 drosophila	Q9ab65 caulobacter	Q14234 homo sapien	Q7z3f5 homo sapien	Q8zne5 salmonella	Q9rkl9 streptomyce	Q8fjt1 escherichia	Q83sal shigella fl	Q8niz0 neurospora	069907 streptomyce	Q9fp71 oryza sativ	Q9su08 arabidopsis	Q8rxd0 arabidopsis	Description

53.5	53.5	53.5	53.5	53.5	53.5	54	54	54	54	54	54.5	55	55	55	55	55	55.5	56	56	56	56	56	56	56	56	56.5	56.5	56.5	
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Submitted (WAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL049640; CAB40995.1; -.
EMBL; AL161534; CAB78320.1; -.
PIR; T06636; T06636.
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T20K18.130 OR AT4G12780.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2003 (TrEMBLrel. 24, 13) (TremBLrel. 24, 13) (TremBLrel. 24, 13)
                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
P0458A05.18 protein (B1157F09.8 protein).
P0458A05.18 OR B1157F09.8.
Oryza sativa (Rice).
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Bevan M., Peters S.A.,
Bancroft I., Mewes H.W
             "Oryza sativa nipponbare(GA3) geno clone:P0458A05.";
                                                                        STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T
                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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2 (TrEMBLrel. 22, Created)
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Best Local
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Nature 417:141-147(2002).
EMBL; AL939124; CAA19411.1; -.
PIR; T34804; T34804.
Hypothetical protein; Complete p.
SEQUENCE 168 AA; 17934 MW; 7.
                                                                                                                                                                                                                                                                    STRAIN=A3(2) / M145;
MEDLINE=2196410; PubMed=12000953;
Bentley S.D. (Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Cronin A., Fraser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, La
01-JUN-2003 (TrEMBLrel. 24, La
Hypothetical protein SCO5619.
SCO5619 OR SCI36.
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"Oryza sativa nipponbare(GA3) genomic
clone:B1157F09.";
Submitted (FEB-2001) to the EMBL/GenB
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SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T
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01-AUG-1998
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Pred. No. 2.7;
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3; Mismatches
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01-JUN-2003
01-JUN-2003
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                                                                                                                                                                     Complete
SEQUENCE
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STRAIN=2457T / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., De
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J.,

Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., &
Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                              "Complete genome sequence and comparative flexneri serctype 2a strain 2457T."; Infect. Immun. 71:2775-2786 (2003). EMBL; AE015086; AAN42202.1; -. EMBL; AE016979; AAP16075.1; -.
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Nucleic
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Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Y., Shen Y., Zhang X., Zhang J., Yang G., Wu H., Yang J., Yang F., Zhang X., Zhang J., Xan B., Ding Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen
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Schulte U., Aign V., H
Syakatura G., Mewes H.
Submitted (JUN-2002) t
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
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Enterobacteriaceae; Shigella.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ
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                                                                       . Similarity
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99309 MW; 5A110FCA4C09D8F9 CRC64;
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73.7%;
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., Mannhaupt G.;
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required for outer membr
                                                                    Score 59; DB
Pred. No. 16;
4; Mismatches
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Qu D., Do
K., Chen
m Y., Hou
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Q9RKL9;
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01-MAY-2000
01-JUN-2003
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Q8FJT1;
01-MAR-2003
                                             MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                    rropable peptidase.
SCO4108 OR SCD17.12
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Extensive mosaic structure revealed by the complete of uropathogenic Escherichia coli."; proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002). EMBL; AE016757; AAN79291.1; -.
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SEQUENCE FROM N.A.
CFT073
                                                                                                                               STRAIN=A3(2);
Thomson N.R., Parkhill
Submitted (SEP-1999) to
                                                                                                                                                                                                        Brown S.P., Harris D.;
Submitted (SEP-1999) t
                                                                                                                                                                                                                                                                               NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor. Bacteria, Actinobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=O6:H1 / CFT073 |/ ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Rowelch R.A., Buckles B.L., Liou S.-R., Boutin A., Hackett Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna Nayhew G.F., Rose D.J., Zhou S., Blattner F.R.;

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
                           Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and
                                                                                                                                                                                                                                  STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; NCBI_TaxID=217992;
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01-OCT-2003
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Mb Streptomyces|coelicolor
Microbiol. 21:77-96(1996).
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Last sequence tast annotated
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EMBL/GenBank/DDBJ databases.
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Hackett J., S
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBZNE5;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative von Willebrand factor, vWF type A domain.
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Nature 417:141-147(2002).
EMBL; AL939118; CAB56389.1; -.
GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002886; Peptidase_M37.
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Complete proteome.
SEQUENCE 347 AA; 35432 MW; 4
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MEDLINE-21534948; PubMed-1167769;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W.,
McClelland M., Sanderson K.E., Spieth J., Clifton S.W.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., N
Leonard S., Sun H., Florea L., Miller W., Stoneking T., Nha
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Waterston R., Wilson R.K.;
                                                                                                                                                         PROSITE; PS00013; PROKAR LIPOPROTEIN; PROSITE; PS50234; VWFA; I.
Hypothetical protein; Complete proteom SEQUENCE 593 AA; 64640 MW; 595CASE
                                                                                                                                                                                                                                                                       Nature 413:852-856(2001).
EMBL; AE008803; AAL21216.1; -.
InterPro; IPR000437; Prok lipoprot
InterPro; IPR002035; VWF A.
Pfam; PF00092; vwa; 1.
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STRAIN=A3(2) / M14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                    SMART; SM00327; VWA;
                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence
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15; Conserv
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                                                                                        Similarity
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S., Layman D.,
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analysis of cloned genomic proc. Natl. Acad. Sci. U.S., SWBL; M17282; AAC98395.1; JEMBL; M17265; AAC98395.1; JEMBL; M17266; AAC98395.1; JEMBL; M17266; AAC98395.1; JEMBL; M17266; AAC98395.1; JEMBL; M17270; AAC98395.1; JEMBL; M17270; AAC98395.1; JEMBL; M17270; AAC98395.1; JEMBL; M17272; AAC98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87274906; PubMed=3038460; Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J., Ornstein-Goldstein N.; "Structure of the 3' region of the human el of Alu repetitive sequences and few coding Connect. Tissue Res. 16:197-211(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                  Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Rosenbloom J.C., Peltonen L., Rosenbloom J.; "Alternative splicing of human elastin mRNA indicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87289668; PubMed=3039501;
Indik Z., Yeh H., Ornstein-Goldst
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01-JUN-2001
01-JUN-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; "Complete genome sequence of Caulobacter crescentus."; "Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
       Q9W2J2
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STRAIN=ATCC 19089 /
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GO; GO:0030023; F:extracellular matrix constituent con:
InterPro; IPR001179; FKBP PPIASE.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00453; FKBP PPIASE 1; 1.
SEQUENCE 757 AA; 66136 MW; 23B7FE5B8AF85CA8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter crescentus. Bacteria; Proteobacteria;
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InterPro; IPR002146; ATPsynt_B/B'sub.
Pfam; PF00430; ATP-synt_B; 1.
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M17274; AAC98395.1; J
M17275; AAC98395.1; J
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M17277; AAC98395.1; J
M17279; AAC98395.1; J
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                                                                                                                    ASAEAAERQAKEEAVLAEKLAAAEA 134
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  RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Celniker S.E., Hit P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Ballew R.M., Basu A., Baxer B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley S.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolchakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bockova D., Betchar A., Dongs M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Glodek A., Gong F., Gorzell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris N., Moshrefi A.,
RA Melson D.R., Nelson K.A., Mobarry C., Morris N., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nobarry C., Morris N., Moshrefi A.,
RA Melson D.R., Nelson K.A., Samders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Sheng X.H., Zhong F., Norler R., Venter J.C.,
RA Sheng X.H., Zhong F., Norler R., Venter J.C.,
RA Sheng X.H., Zhong F., Norler R., Venter J.C.,
RA Sheng X.H., Zhong F., Norler R., Venter J.C.,
RA Shiba R.A., Myers E.M., Rabin G.M., Venter J.C.,
RA Shiba R.A., Myers E.M., Shib
                                                             RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Holder M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Houanenavong S., Pittman G.S., Parel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O.,
Stapleton M., Strong R., Svirskas R., Tector C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2002
01-OCT-2003
CG18375 prot
SEQUENCE FROM N./
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Eukaryota; Metazoa; Arthropoda; Hexaspoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Bayraktaroglu L., Campbell K.,

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Pfam; PF00018; SH3; 1.

ProDom; PD000066; SH3; 1.

SMART; SM00248; ANK; 2.

SMART; SM00326; SH3; 1.

PROSITE; PS50008; ANK REPEAT; 2.

PROSITE; PS50029; ANK REP REGION; 1.

PROSITE; PS50029; SH3; 1.

ANK repeat; Repeat.

SEQUENCE 997 AA; 107821 MW; E711
                                      Submitted (JAN-2003) to the ENEL; BT003215; AA024970.1; -
InterPro; IPR002110; ANK.
InterPro; IPR001452; SH3.
Pfam; PF00023; ank; 2.
Pfam; PF00018; SH3; 1.
ProDom; PD000066; SH3; 1.
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                                                                                                                                                                                                                                   STRAIN=y;
STRAIN=y;
Strapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.
Miranda A., Mungall C.J., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                         Miranda A., Munyu...
Miranda A., Phouanenavong
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InterPro; IPR002110; ANK.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2003
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01-JUN-2003
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Q13625; 1YCS.
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د <u>د</u>
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Last annotation update)
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                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB Pred. No. 67; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E712D400C2C4FD3D CRC64;
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databases.
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Park S.,
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QRESULT TO RESULT TO RESUL
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RA Adams N.D., Celniker S.E., Holt R.A., Shburner M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Holt R.A., Shburner M., Henderson S.N.,
RA Brandon R.C., Nortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Change M., Ffeiffer B.D.,
RA Barid J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butter H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butter H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pieischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Herinandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Herinandez J.R., Ketchum K.A.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Davies M.,
RA Melson D.R., Nelson K.A., Nixon K., Nussexn D.R., Palebon D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nussexn D.R., Shen H.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Reinert E., Spradling A.C., Stapleton M., Skupski M.P., Shen H.,
RA Mang S.M., Woodaget, Morris J., Shan M., Strong R., Sun E.,
RA Williams S.M., Woodaget, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Glibbs R.A., Myers B.M., Rubin G.M., Venter E., Wang A.H., Wang X.,
RA Glibbs R.A., Myers B.M., Rubin G.M., Venter J.C.,
RA Glibbs R.A., Myers B.M., Rubin G.M., Venter J.C.,
RA Glibbs R.A., Myers B.M., Rubin G.M., Venter J.C.,
RA Glibbs R.A., Myers B.M., Rubin G.M., Venter J.C.,
RA Glibbs R.A., Myers B.M., Rubin G.M., Venter J.C.,
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Best Local Similarity
Matches 15; Conserv
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Q86BG1;
Q86BG1;
O1-JUN-2003
O1-JUN-2003
O1-OCT-2003
CG18375-PB.
CG18375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI _TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
PROSITE;
PROSITE;
SEQUENCE
  SEQUENCE FROM Misra S., Cro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                 genome sequence of Dro
nce 287:2185-2195(2000)
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                                                           FROM
FROM N.A.
Crosby M.
P., Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020 AA;
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  Y.A
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25,
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Last annotation updat
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     S
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No.
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69;
  Bayraktaroglu L., Campbell Prochnik S.E., Smith C.D.,
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Search completed: April 20, 2004, 22:00:27 Job time : 41 secs
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

R InterPro; IPRO02110; ANX.

R InterPro; IPR002110; ANX.

R InterPro; IPR001452; SH3.

R Pfam; PF000023; ank; 2.

R Pfam; PF000018; SH3; 1.

R ProDom; PD000106; SH3; 1.

R ProDom; PM00248; ANX; 2.

R SMART; SM00248; ANX; 2.

R SMART; SM0026; SH3; 1.

R SMART; SM00326; SH3; 1.

R PROSITE; PS5008; ANX REPEAT; 2.

R PROSITE; PS50027; ANX REP REGION; 1.

R PROSITE; PS50002; SH3; 1.

R PROSITE; PS50002; SH3; 1.
                                                                                                                                 Query Match 54.3%;
Best Local Similarity 60.0%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

FlyBase;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewis S.E.;
                                                              1 АХАЕААЕКААКҮААЕААЕКААКАХА 25
                                                                                                                                   2; Mismatches
                                                                                                                                                   Score 57; DB 5; Length 1069; Pred. No. 72;
                                                                                                                                   8; Indels
                                                                                                                                   0;
                                                                                                                                   Gaps
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